

In the Claims

Please amend the claims presented during the international phase as follows.

Applicant presents a full set of claims showing markups of the claims with insertions and deletions indicated by underlining and strikethrough text, respectively.

1.-17. (Canceled)

18. (New) A method for identifying a compound useful in the prevention and/or treatment of metabolic diseases, comprising the steps of:

a) contacting a protein or polypeptide encoded by a T17E9.1a/*kin-18* gene or an ortholog thereof with a test chemical, in such a way that a signal is generated that is representative for the interaction between said test chemical and said protein or polypeptide; and

b) detecting the signal thus generated, said signal identifying a compound that modulates said protein or polypeptide, which is indicative that the compound is useful for the prevention and/or treatment of metabolic diseases.

19. (New) The method of claim 18, wherein the ortholog is a human *JNK/SAPK* inhibitory kinase (*JIK*) gene, a prostate derived *STE20*-like kinase (*PSK* or *TAO2*) gene, or a thousand and one amino acid protein kinase gene (*TAO1* and *Q9P2I6*).

20. (New) The method of claim 18, wherein the T17E9.1a/*kin-18* gene or ortholog thereof encodes a protein or polypeptide comprising one of the amino acid sequences of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8 and SEQ ID NO: 10; or an analog, variant, allele or ortholog that has 95% or more sequence identity with SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8 or SEQ ID NO: 10; or a part, fragment or truncated version comprising a kinase domain thereof.

21. (New) The method of claim 18, wherein the T17E9.1a/*kin-18* gene or ortholog thereof is a nucleic acid comprising the nucleotide sequence of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7 or SEQ ID NO: 9; or a mutant, variant, allele, analog or ortholog that has 95% or more sequence identity with SEQ ID NO: 1, SEQ ID NO: 3, SEQ

ID NO: 5, SEQ ID NO: 7 or SEQ ID NO: 9; or a part, fragment or truncated version encoding a kinase domain thereof.

22. (New) The method of claim 18, further comprising comparing the signal generated to a signal generated by a control assay.

23. (New) The method of claim 20, wherein the kinase domain comprises amino acid residues 30 to 289 of SEQ ID NO:2, amino acid residues 24 to 277 of SEQ ID NO:4, amino acid residues 28 to 281 of SEQ ID NO:6, amino acid residues 28 to 281 of SEQ ID NO:8, or amino acid residues 32 to 285 of SEQ ID NO:10.

24. (New) A method for identifying a compound useful in the prevention and/or treatment of metabolic diseases, comprising the steps of:

a) contacting host cells or organisms transformed with and/or containing a T17E9.1a/*kin-18* nucleic acid sequence or an ortholog thereof, which nucleic acid sequence or ortholog expresses and/or produces a T17E9.1a/*kin-18* or orthologous amino acid sequence, with a test chemical, in such a way that a signal is generated that is representative for the interaction between said test chemical and said protein or polypeptide; and

b) detecting the signal thus generated, said signal identifying a compound that modulates said protein or polypeptide, which is indicative that the compound is useful for the prevention and/or treatment of metabolic diseases.

25. (New) The method of claim 24, wherein the ortholog is a human *JNK/SAPK* inhibitory kinase (*JIK*) gene, a prostate derived *STE20*-like kinase (*PSK* or *TAO2*) gene, or a thousand and one amino acid protein kinase gene (*TAO1* and *Q9P2I6*).

26. (New) The method of claim 24, wherein the T17E9.1a/*kin-18* or orthologous amino acid sequence comprises SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8 or SEQ ID NO: 10; or an analog, variant, allele or ortholog that has 95% or more sequence identity with SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8 or SEQ ID NO: 10; or a part, fragment or truncated version comprising a kinase domain thereof.

27. (New) The method of claim 24, wherein the T17E9.1a/*kin-18* gene or ortholog thereof is a nucleic acid comprising the nucleotide sequence of SEQ ID NO: 1, SEQ ID NO:

3, SEQ ID NO: 5, SEQ ID NO: 7 or SEQ ID NO: 9; or a mutant, variant, allele, analog or ortholog that has 95% or more sequence identity with SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7 or SEQ ID NO: 9; or a part, fragment or truncated version encoding a kinase domain thereof.

28. (New) The method of claim 24, further comprising comparing the signal generated to a signal generated by a control assay.

29. (New) The method of claim 26, wherein the kinase domain comprises amino acid residues 30 to 289 of SEQ ID NO:2, amino acid residues 24 to 277 of SEQ ID NO:4, amino acid residues 28 to 281 of SEQ ID NO:6, amino acid residues 28 to 281 of SEQ ID NO:8, or amino acid residues 32 to 285 of SEQ ID NO:10.